SEQUENCE LISTING

<110> Houston, Michael E.
Hodges, Robert

<120> Use of Coiled-Coil Structural Scaffold to Generate Structure-Specific Peptides

<130> 003592-007

<150> US 60/211,892
<151> 2000-06-14

<150> US 60/213,387
<151> 2000-06-23

<160> 16

<170> PatentIn version 3.0

<210> 1
<211> 619
<212> PRT
<213> Streptococcus pneumoniae

<400> 1

Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile
1 5 10 15

Leu Gly Ala Gly Phe Val Ala Ser Gln Pro Thr Val Val Arg Ala Glu
20 25 30

Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala
35 40 45

Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala Gln
50 55 60

Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp
65 70 75 80

Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu
85 90 95

Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr
100 105 110

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Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met Ile
        115                 120                 125

Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr
    130                 135                 140

Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys
145                 150                 155                 160

Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys
                165                 170                 175

Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr
            180                 185                 190

Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala Lys
        195                 200                 205

Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu Lys
    210                 215                 220

Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg
225                 230                 235                 240

Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys
                245                 250                 255

Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala
            260                 265                 270

Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Asn Val Glu
        275                 280                 285

Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala
    290                 295                 300

Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu Pro
305                 310                 315                 320

Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala
                325                 330                 335

Glu Gln Pro Lys Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys
            340                 345                 350

Pro Glu Lys Pro Ala Glu Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln
        355                 360                 365
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Gln Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg
370 375 380

Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro
385 390 395 400

Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
405 410 415

Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr
420 425 430

Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn
435 440 445

Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp
450 455 460

Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met
465 470 475 480

Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala
485 490 495

Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr
500 505 510

Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn
515 520 525

Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp
530 535 540

Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met
545 550 555 560

Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala
565 570 575

Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp
580 585 590

Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp
595 600 605

Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp Val
610 615

<210> 2
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> stabilizing strand

<220>
<221> MOD_RES
<222> (2)
<223> Nle

<400> 2

Cys Xaa Gly Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala
1 5 10 15

Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys
20 25 30

Lys Glu Ile Glu Ala Leu Lys Lys
35 40

<210> 3
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> hybrid sequence

<220>
<221> MOD_RES
<222> (2)
<223> Nle

<400> 3

Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln
1 5 10 15

Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile
20 25 30

Lys Glu Leu Asp Glu Ser

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<210> 4
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (2)
<223> Nle

<400> 4

Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln
1 5 10 15

Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu
20 25 30

Lys Glu Ile Asp Glu Ser
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<210> 5
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> PEPTIDE
<222> (4)..(20)
<223> Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any a
mino
acid

<400> 5

Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa
1 5 10 15

Leu Glu Lys Xaa
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<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 6

Glu Glu Leu Ser Asp Lys Ile Asp
1 5

<210> 7
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> hybrid sequence

<220>
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<223> Nle

<400> 7

Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Lys Ile Glu Glu Leu Ser
1 5 10 15

Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys
20 25

<210> 8
<211> 21
<212> PRT
<213> Haemophilus influenzae

<400> 8

Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser
1 5 10 15

Asn Leu Thr Ser Ala
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<210> 9
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> hybrid sequence

<400> 9

Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln
1 5 10 15

Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly
20 25

<210> 10
<211> 20
<212> PRT
<213> Streptococcus pneumoniae

<400> 10

Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala
1 5 10 15

Glu Gln Val Leu
20

<210> 11
<211> 15
<212> PRT
<213> Streptococcus pneumoniae

<400> 11

Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp
1 5 10 15

<210> 12
<211> 10
<212> PRT
<213> Streptococcus pneumoniae

<400> 12

Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys
1 5 10

<210> 13
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> hybrid sequence

<400> 13

Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu
1 5 10 15

Lys Asp Ala Glu Thr Asn Asn Val Glu Asp Ala Lys Lys Gln Thr Glu
20 25 30

Leu Glu Lys
35

<210> 14
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> hybrid sequence

<400> 14

Asp Ile Glu Asp Leu Lys Asn Ser Ile Gly Glu Leu Glu Asp Asn Ile
1 5 10 15

Lys Glu Leu Glu Thr Asn Ile Val Glu Leu Ala Lys Lys Ile Thr Glu
20 25 30

Leu Glu Lys
35

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Coiled-coil scaffold

<220>

<221> PEPTIDE
<222> (1)
<223> Amino acid 1 is Xaa wherein Xaa = A and A can be I, L or V.

<220>
<221> PEPTIDE
<222> (2)..(7)
<223> Amino acids 2, 3, 5-7 are Xaa wherein Xaa = any amino acid.

<220>
<221> PEPTIDE
<222> (4)
<223> Amino acid 4 is Xaa wherein Xaa = D and D can be I, L or V.

<220>
<221> PEPTIDE
<222> (1)..(7)
<223> Amino acids 1-7 can be repeated one or more times.

<400> 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Coiled-coil scaffold

<220>
<221> MOD_RES
<222> (2)
<223> Nle

<220>
<221> PEPTIDE
<222> (5)..(10)
<223> Amino acids 5, 6, and 8-10 are Xaa wherein Xaa = any amino a
cid.

<220>
<221> PEPTIDE
<222> (4)..(10)
<223> Amino acids 4-10 can be repeated one or more times.

<400> 16

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Cys Xaa Gly Ile Xaa Xaa Leu Xaa Xaa Xaa
1               5                   10
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